SEQUENCE LISTING

<110> Baum, Peter Robert
Fanslow III, William C.

<120> Molecules Designated LDCAM

<130> 2873-US

<140> to be assigned--
<141> 2001-02-06

<140> PCT/US99/17905
<141> 1999-08-05

<150> 60/095,672
<151> 1998-08-07

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<170> PatentIn Ver. 2.0

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Ala Ala Ala Ala Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu
          15                  20                  25

ctg ctg ttg ctc ttc tcc gcc gcg gca ctg atc ccc aca ggt gat ggg   147
Leu Leu Leu Leu Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly
     30                  35                  40

cag aat ctg ttt acg aaa gac gtg aca gtg atc gag gga gag gtt gcg   195
Gln Asn Leu Phe Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala
 45                  50                  55                  60

acc atc agt tgc caa gtc aat aag agt gac gac tct gtg att cag cta   243
Thr Ile Ser Cys Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu
                 65                  70                  75

ctg aat ccc aac agg cag acc att tat ttc agg gac ttc agg cct ttg   291
Leu Asn Pro Asn Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu
             80                  85                  90

aag gac agc agg ttt cag ttg ctg aat ttt tct agc agt gaa ctc aaa   339
Lys Asp Ser Arg Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys
          95                  100                 105

gta tca ttg aca aac gtc tca att tct gat gaa gga aga tac ttt tgc   387
Val Ser Leu Thr Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys
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Gln Leu Tyr Thr Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val
125                 130                 135                 140

ctg gtc cca cca cgt aat ctg atg atc gat atc cag aaa gac act gcg   483
Leu Val Pro Pro Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala
                145                 150                 155

gtg gaa ggt gag gag att gaa gtc aac tgc act gct atg gcc agc aag   531
Val Glu Gly Glu Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys
            160                 165                 170

cca gcc acg act atc agg tgg ttc aaa ggg aac aca gag cta aaa ggc   579
Pro Ala Thr Thr Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly
        175                 180                 185

aaa tcg gag gtg gaa gag tgg tca gac atg tac act gtg acc agt cag   627
Lys Ser Glu Val Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln
    190                 195                 200

ctg atg ctg aag gtg cac aag gag gac gat ggg gtc cca gtg atc tgc   675
Leu Met Leu Lys Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys
205                 210                 215                 220

cag gtg gag cac cct gcg gtc act gga aac ctg cag acc cag cgg tat   723
Gln Val Glu His Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr
                225                 230                 235

cta gaa gta cag tat aag cct caa gtg cac att cag atg act tat cct   771
Leu Glu Val Gln Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro
            240                 245                 250

cta caa ggc tta acc cgg gaa ggg gac gcg ctt gag tta aca tgt gaa   819
Leu Gln Gly Leu Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu
        255                 260                 265

gcc atc ggg aag ccc cag cct gtg atg gta act tgg gtg aga gtc gat   867
Ala Ile Gly Lys Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp
    270                 275                 280

gat gaa atg cct caa cac gcc gta ctg tct ggg ccc aac ctg ttc atc   915
Asp Glu Met Pro Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile
285                 290                 295                 300

aat aac cta aac aaa aca gat aat ggt aca tac cgc tgt gaa gct tca   963
Asn Asn Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser
                305                 310                 315

aac ata gtg ggg aaa gct cac tcg gat tat atg ctg tat gta tac gat  1011
Asn Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp
            320                 325                 330

ccc ccc aca act atc cct cct ccc aca aca acc acc acc acc acc acc  1059
Pro Pro Thr Thr Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr
        335                 340                 345

acc acc acc acc acc atc ctt acc atc atc aca gat tcc cga gca ggt  1107
Thr Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly
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gaa gaa ggc tcg atc agg gca gtg gat cat gcc gtg atc ggt ggc gtc  1155
Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val
365                 370                 375                 380

gtg gcg gtg gtg gtg ttc gcc atg ctg tgc ttg ctc atc att ctg ggg  1203
Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly
                385                 390                 395
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cgc tat ttt gcc aga cat aaa ggt aca tac ttc act cat gaa gcc aaa  1251
Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys
            400                 405                 410

gga gcc gat gac gca gca gac gca gac aca gct ata atc aat gca gaa  1299
Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
        415                 420                 425

gga gga cag aac aac tcc gaa gaa aag aaa gag tac ttc atc          1341
Gly Gly Gln Asn Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile
    430                 435                 440

tagatcagcc tttttgtttc aatgaggtgt ccaactggcc ctatttagat gataaagaga  1401

cagtgatatt ggaacttgcg agaaattcgt gtgttttttt atgaatgggt ggaaaggtgt  1461

gagactggga aggcttggga tttgctgtgt aaaaaaaaaa aaaaaatgtt ctttggaaag  1521

aaaaaagcgg ccgctttctt attctatttc aacattcagc ttaatcataa tcctaaaatc  1581

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Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe
         35                  40                  45

Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys
     50                  55                  60

Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn
 65                  70                  75                  80

Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg
                 85                  90                  95

Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr
            100                 105                 110

Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr
        115                 120                 125

Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro
    130                 135                 140

Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu
145                 150                 155                 160

Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr
                165                 170                 175

Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val
            180                 185                 190
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Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys
        195                 200                 205

Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His
    210                 215                 220

Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln
225                 230                 235                 240

Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu
                245                 250                 255

Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys
            260                 265                 270

Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro
        275                 280                 285

Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn
    290                 295                 300

Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly
305                 310                 315                 320

Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr
                325                 330                 335

Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr
            340                 345                 350

Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Ser
        355                 360                 365

Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val Val Ala Val Val
    370                 375                 380

Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala
385                 390                 395                 400

Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp
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Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn
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    1               5                  10                  15

tcg gcc gcg gca ctg atc ccc aca ggt gat gga cag aat ctg ttt act  94
Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe Thr
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                    20                  25                  30

aaa gac gtg aca gtg att gaa gga gaa gtg gca acc atc agc tgc cag  142
Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys Gln
               35                  40                  45

gtc aat aag agt gac gac tca gtg atc cag ctc ctg aac ccc aac agg  190
Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn Arg
          50                  55                  60

cag acc att tac ttc agg gac ttc agg cct ttg aag gac agc agg ttt  238
Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg Phe
      65                  70                  75

cag ctg ctg aat ttt tct agc agt gaa ctc aaa gtg tca ctg acg aat  286
Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr Asn
  80                  85                  90                  95

gtc tca atc tcg gat gaa ggg aga tac ttc tgc cag ctc tac acg gac  334
Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr Asp
                 100                 105                 110

ccc cca cag gag agt tac acc acc atc aca gtc ctg gtt cct cca cgt  382
Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro Arg
             115                 120                 125

aac ttg atg atc gat atc cag aaa gac acg gca gtt gaa ggg gag gag  430
Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu Glu
         130                 135                 140

att gaa gtc aac tgt act gcc atg gcc agc aag cca gcg acg acc atc  478
Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr Ile
     145                 150                 155

agg tgg ttc aaa ggg aac aag gaa ctc aaa ggc aaa tca gag gtg gag  526
Arg Trp Phe Lys Gly Asn Lys Glu Leu Lys Gly Lys Ser Glu Val Glu
160                 165                 170                 175

gag tgg tcg gac atg tac act gtg acc agt cag ctg atg ctg aag gtg  574
Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val
                 180                 185                 190

cac aag gag gac gac ggg gtc ccg gtg atc tgc cag gtg gag cac cct  622
His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His Pro
             195                 200                 205

gcg gtc act gga aac ctg cag acc cag cgc tat cta gaa gtg cag tat  670
Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr
         210                 215                 220

aaa ccg caa gtg cat atc cag atg act tac cct ctg caa ggc cta acc  718
Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr
     225                 230                 235

cgg gaa ggg gat gca ttt gag tta acg tgt gaa gcc atc ggg aag ccc  766
Arg Glu Gly Asp Ala Phe Glu Leu Thr Cys Glu Ala Ile Gly Lys Pro
240                 245                 250                 255

cag cct gtg atg gta act tgg gtg aga gtc gat gat gaa atg cct caa  814
Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro Gln
                 260                 265                 270

cat gcc gta ctg tct ggg cca aac ctg ttc atc aat aac cta aac aaa  862
His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn Lys
             275                 280                 285

aca gat aac ggt act tac cgc tgt gag gct tcc aac ata gtg gga aag  910
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Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly Lys
        290                 295                 300

gct cat tcg gac tat atg ctg tat gta tac gat ccc ccc aca act atc  958
Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr Ile
    305                 310                 315

cct cct ccc aca aca acc acc acc act acc acc acc acc acc acc acc  1006
Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr
320                 325                 330                 335

atc ctt acc atc atc aca gat tct cga gca ggt gaa gag ggg acc att  1054
Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Thr Ile
                340                 345                 350

ggg gca gtg gac cac gca gtg att ggt ggc gtc gta gcc gtg gtg gtg  1102
Gly Ala Val Asp His Ala Val Ile Gly Gly Val Val Ala Val Val Val
            355                 360                 365

ttt gcc atg cta tgc ttg ctc atc att ctg ggc cgc tat ttt gcc aga  1150
Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala Arg
        370                 375                 380

cat aaa ggt aca tac ttc act cat gaa gcc aaa gga gcc gat gac gca  1198
His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp Ala
    385                 390                 395

gca gac gca gac aca gct ata atc aat gca gaa gga gga cag aac aac  1246
Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn
400                 405                 410                 415

tcc gaa gaa aag aaa gag tac ttc at ctagatcagc ctttttgttc         1292
Ser Glu Glu Lys Lys Glu Tyr Phe
                420

caatgaggtg tccaactggc ctgtttagat gataaagaga cagtgatact ggaactttcg  1352

agaagctcgt gtggtttttt gttttgtttt gttttttttat gagtgggtgg agagatgcga  1412

gactgggaag gcttgggatt tgcaatgtac aaacaaaaac aaagaatgtt ctttgaaagt  1472

acactctgct gtttgacacc tctttttaat ctggttttaa tttgctttgg gttttgggtt  1532

tttttggttt tttgtttttt tcatttatat ttcttcctac caagtcaaac ttgggtactt  1592

ggatttggtt tcggtagatt gcagaaaatt ctgtgccttg tttttcattc gtttgttgtg  1652

tttcttccct cttgcccatt tatttttccc aaaatcaaat ttgttttttt ccccctccca  1712

aacctcccat tttttggaat tgacctgctg gaattcctaa gactttctcc ctgttgccag  1772

tttcttttat ttgtgttaac ggtgactgct ttctgttcca aattcagttt cataaaagga  1832

aaaccagcac aatttagatt tcatagttca gaatttagtg tctccatgat gcatccttct  1892

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Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys Gln Val
        35                  40                  45
Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn Arg Gln
    50                  55                  60
Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg Phe Gln
65                  70                  75                  80
Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr Asn Val
                85                  90                  95
Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr Asp Pro
            100                 105                 110
Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro Arg Asn
        115                 120                 125
Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu Glu Ile
    130                 135                 140
Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr Ile Arg
145                 150                 155                 160
Trp Phe Lys Gly Asn Lys Glu Leu Lys Gly Lys Ser Glu Val Glu Glu
                165                 170                 175
Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val His
            180                 185                 190
Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His Pro Ala
        195                 200                 205
Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr Lys
    210                 215                 220
Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr Arg
225                 230                 235                 240
Glu Gly Asp Ala Phe Glu Leu Thr Cys Glu Ala Ile Gly Lys Pro Gln
                245                 250                 255
Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro Gln His
            260                 265                 270
Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn Lys Thr
        275                 280                 285
Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly Lys Ala
    290                 295                 300
His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr Ile Pro
305                 310                 315                 320
Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Ile
                325                 330                 335
Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Thr Ile Gly
            340                 345                 350
Ala Val Asp His Ala Val Ile Gly Gly Val Val Ala Val Val Val Phe
        355                 360                 365
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Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala Arg His
    370                 375                 380

Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala
385                 390                 395                 400

Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn Ser
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Glu Glu Lys Lys Glu Tyr Phe
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gccagcgccc agccagggag ccggccggga agcgcg atg ggg gcc cca gcc gcc 174
                                        Met Gly Ala Pro Ala Ala
                                          1   5

tcg ctc ctg ctc ctg ctc ctg ctg ttc gcc tgc tgc tgg gcg ccc ggc 222
Ser Leu Leu Leu Leu Leu Leu Leu Phe Ala Cys Cys Trp Ala Pro Gly
            10   15   20

ggg gcc aac ctc tcc cag gac ggc tac tgg cag gag cag gat ttg gag 270
Gly Ala Asn Leu Ser Gln Asp Gly Tyr Trp Gln Glu Gln Asp Leu Glu
        25   30   35

ctg gga act ctg gct cca ctc gac gag gcc atc agc tcc aca gtc tgg 318
Leu Gly Thr Leu Ala Pro Leu Asp Glu Ala Ile Ser Ser Thr Val Trp
    40   45   50

agc agc cct gac atg ctg gcc agt caa gac agc cag ccc tgg aca tct 366
Ser Ser Pro Asp Met Leu Ala Ser Gln Asp Ser Gln Pro Trp Thr Ser

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 55                  60                  65                  70

gat gaa aca gtg gtg gct ggt ggc acc gtg gtg ctc aag tgc caa gtg  414
Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu Lys Cys Gln Val
                 75                  80                  85

aaa gat cac gag gac tca tcc ctg caa tgg tct aac cct gct cag cag  462
Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn Pro Ala Gln Gln
             90                  95                 100

act ctc tac ttt ggg gag aag aga gcc ctt cga gat aat cga att cag  510
Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp Asn Arg Ile Gln
        105                 110                 115

ctg gtt acc tct acg ccc cac gag ctc agc atc agc atc agc aat gtg  558
Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser Ile Ser Asn Val
    120                 125                 130

gcc ctg gca gac gag ggc gag tac acc tgc tca atc ttc act atg cct  606
Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile Phe Thr Met Pro
135                 140                 145                 150

gtg cga act gcc aag tcc ctc gtc act gtg cta gga att cca cag aag  654
Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly Ile Pro Gln Lys
                155                 160                 165

ccc atc atc act ggt tat aaa tct tca tta cgg gaa aaa gac aca gcc  702
Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu Lys Asp Thr Ala
            170                 175                 180

acc cta aac tgt cag tct tct ggg agc aag cct gca gcc cgg ctc acc  750
Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala Ala Arg Leu Thr
        185                 190                 195

tgg aga aag ggt gac caa gaa ctc cac gga gaa cca acc cgc ata cag  798
Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro Thr Arg Ile Gln
    200                 205                 210

gaa gat ccc aat ggt aaa acc ttc act gtc agc agc tcg gtg aca ttc  846
Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser Ser Val Thr Phe
215                 220                 225                 230

cag gtt acc cgg gag gat gat ggg gcg agc atc gtg tgc tct gtg aac  894
Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val Cys Ser Val Asn
                235                 240                 245

cat gaa tct cta aag gga gct gac aga tcc acc tct caa cgc att gaa  942
His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser Gln Arg Ile Glu
            250                 255                 260

gtt tta tac aca cca act gcg atg att agg cca gac cct ccc cat cct  990
Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp Pro Pro His Pro
        265                 270                 275

cgt gag ggc cag aag ctg ttg cta cac tgt gag ggt cgc ggc aat cca 1038
Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly Arg Gly Asn Pro
    280                 285                 290

gtc ccc cag cag tac cta tgg gag aag gag ggc agt gtg cca ccc ctg 1086
Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser Val Pro Pro Leu
295                 300                 305                 310

aag atg acc cag gag agt gcc ctg atc ttc cct ttc ctc aac aag agt 1134
Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe Leu Asn Lys Ser
                315                 320                 325

gac agt ggc acc tac ggc tgc aca gcc acc agc aac atg ggc agc tac 1182
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Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn Met Gly Ser Tyr
            330                 335                 340

aag gcc tac tac acc ctc aat gtt aat gac ccc agt ccg gtg ccc tcc  1230
Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser Pro Val Pro Ser
        345                 350                 355

tcc tcc agc acc tac cac gcc atc atc ggt ggg atc gtg gct ttc att  1278
Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile Val Ala Phe Ile
    360                 365                 370

gtc ttc ctg ctg ctc atc atg ctc atc ttc ctt ggc cac tac ttg atc  1326
Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly His Tyr Leu Ile
375                 380                 385                 390

cgg cac aaa gga acc tac ctg aca cat gag gca aaa ggc tcc gac gat  1374
Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys Gly Ser Asp Asp
                395                 400                 405

gct cca gac gcg gac acg gcc atc atc aat gca gaa ggc ggg cag tca  1422
Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Ser
            410                 415                 420

gga ggg gac gac aag aag gaa tat ttc atc tagaggcgcc tgcccacttc    1472
Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
        425                 430

ctgcgccccc caggggccct gtggggactg ctggggccgt caccaacccg gacttgtaca 1532

gagcaaccgc agggccgccc ctcccgcttg ctccccagcc cacccacccc cctgtacaga 1592

atgtctgctt tgggtgcggt tttgtactcg gtttggaatg gggagggagg agggcggggg 1652

gaggggaggg ttgccctcag ccctttccgt ggcttctctg catttgggtt attattattt 1712

ttgtaacaat cccaaatcaa atctgtctcc aggctggaga ggcaggagcc ctggggtgag 1772

aaaagcaaaa aacaaacaaa aaaaaaaaaa aaaaattcct gcggccgc              1820
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<210> 8
<211> 432
<212> PRT
<213> Homo sapien

<400> 8

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Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Leu Phe Ala
  1               5                  10                  15

Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Gly Tyr Trp
             20                  25                  30

Gln Glu Gln Asp Leu Glu Leu Gly Thr Leu Ala Pro Leu Asp Glu Ala
         35                  40                  45

Ile Ser Ser Thr Val Trp Ser Ser Pro Asp Met Leu Ala Ser Gln Asp
     50                  55                  60

Ser Gln Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val
 65                  70                  75                  80

Val Leu Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp
                 85                  90                  95

Ser Asn Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu
            100                 105                 110
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Arg Asp Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser
115 120 125

Ile Ser Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys
130 135 140

Ser Ile Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val
145 150 155 160

Leu Gly Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu
165 170 175

Arg Glu Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys
180 185 190

Pro Ala Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly
195 200 205

Glu Pro Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val
210 215 220

Ser Ser Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser
225 230 235 240

Ile Val Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser
245 250 255

Thr Ser Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg
260 265 270

Pro Asp Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys
275 280 285

Glu Gly Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu
290 295 300

Gly Ser Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe
305 310 315 320

Pro Phe Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr
325 330 335

Ser Asn Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp
340 345 350

Pro Ser Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly
355 360 365

Gly Ile Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe
370 375 380

Leu Gly His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu
385 390 395 400

Ala Lys Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn
405 410 415

Ala Glu Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
420 425 430

<210> 9
<211> 1718
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> 157..1350

<400> 9

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ctttcggtca acatcgtagt ccacccccctc cccatcccca gcccccgggg attcaggctc 120

gccagcgccc agccagggag ccggccggga agcgcg atg ggg gcc cca gcc gcc 174
Met Gly Ala Pro Ala Ala
1 5

tcg ctc ctg ctc ctg ctc ctg ctg ttc gcc tgc tgc tgg gcg ccc ggc 222
Ser Leu Leu Leu Leu Leu Leu Leu Phe Ala Cys Cys Trp Ala Pro Gly
10 15 20

ggg gcc aac ctc tcc cag gac gac agc cag ccc tgg aca tct gat gaa 270
Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln Pro Trp Thr Ser Asp Glu
25 30 35

aca gtg gtg gct ggt ggc acc gtg gtg ctc aag tgc caa gtg aaa gat 318
Thr Val Val Ala Gly Gly Thr Val Val Leu Lys Cys Gln Val Lys Asp
40 45 50

cac gag gac tca tcc ctg caa tgg tct aac cct gct cag cag act ctc 366
His Glu Asp Ser Ser Leu Gln Trp Ser Asn Pro Ala Gln Gln Thr Leu
55 60 65 70

tac ttt ggg gag aag aga gcc ctt cga gat aat cga att cag ctg gtt 414
Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp Asn Arg Ile Gln Leu Val
75 80 85

acc tct acg ccc cac gag ctc agc atc agc atc agc aat gtg gcc ctg 462
Thr Ser Thr Pro His Glu Leu Ser Ile Ser Ile Ser Asn Val Ala Leu
90 95 100

gca gac gag ggc gag tac acc tgc tca atc ttc act atg cct gtg cga 510
Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile Phe Thr Met Pro Val Arg
105 110 115

act gcc aag tcc ctc gtc act gtg cta gga att cca cag aag ccc atc 558
Thr Ala Lys Ser Leu Val Thr Val Leu Gly Ile Pro Gln Lys Pro Ile
120 125 130

atc act ggt tat aaa tct tca tta cgg gaa aaa gac aca gcc acc cta 606
Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu Lys Asp Thr Ala Thr Leu
135 140 145 150

aac tgt cag tct tct ggg agc aag cct gca gcc cgg ctc acc tgg aga 654
Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala Ala Arg Leu Thr Trp Arg
155 160 165

aag ggt gac caa gaa ctc cac gga gaa cca acc cgc ata cag gaa gat 702
Lys Gly Asp Gln Glu Leu His Gly Glu Pro Thr Arg Ile Gln Glu Asp
170 175 180

ccc aat ggt aaa acc ttc act gtc agc agc tcg gtg aca ttc cag gtt 750
Pro Asn Gly Lys Thr Phe Thr Val Ser Ser Ser Val Thr Phe Gln Val
185 190 195

acc cgg gag gat gat ggg gcg agc atc gtg tgc tct gtg aac cat gaa 798
Thr Arg Glu Asp Asp Gly Ala Ser Ile Val Cys Ser Val Asn His Glu
200 205 210

tct cta aag gga gct gac aga tcc acc tct caa cgc att gaa gtt tta 846

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Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser Gln Arg Ile Glu Val Leu
215                 220                 225                 230

tac aca cca act gcg atg att agg cca gac cct ccc cat cct cgt gag   894
Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp Pro Pro His Pro Arg Glu
                235                 240                 245

ggc cag aag ctg ttg cta cac tgt gag ggt cgc ggc aat cca gtc ccc   942
Gly Gln Lys Leu Leu Leu His Cys Glu Gly Arg Gly Asn Pro Val Pro
            250                 255                 260

cag cag tac cta tgg gag aag gag ggc agt gtg cca ccc ctg aag atg   990
Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser Val Pro Pro Leu Lys Met
        265                 270                 275

acc cag gag agt gcc ctg atc ttc cct ttc ctc aac aag agt gac agt   1038
Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe Leu Asn Lys Ser Asp Ser
    280                 285                 290

ggc acc tac ggc tgc aca gcc acc agc aac atg ggc agc tac aag gcc   1086
Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn Met Gly Ser Tyr Lys Ala
295                 300                 305                 310

tac tac acc ctc aat gtt aat gac ccc agt ccg gtg ccc tcc tcc tcc   1134
Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser Pro Val Pro Ser Ser Ser
                315                 320                 325

agc acc tac cac gcc atc atc ggt ggg atc gtg gct ttc att gtc ttc   1182
Ser Thr Tyr His Ala Ile Ile Gly Gly Ile Val Ala Phe Ile Val Phe
            330                 335                 340

ctg ctg ctc atc atg ctc atc ttc ctt ggc cac tac ttg atc cgg cac   1230
Leu Leu Leu Ile Met Leu Ile Phe Leu Gly His Tyr Leu Ile Arg His
        345                 350                 355

aaa gga acc tac ctg aca cat gag gca aaa ggc tcc gac gat gct cca   1278
Lys Gly Thr Tyr Leu Thr His Glu Ala Lys Gly Ser Asp Asp Ala Pro
    360                 365                 370

gac gcg gac acg gcc atc atc aat gca gaa ggc ggg cag tca gga ggg   1326
Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Ser Gly Gly
375                 380                 385                 390

gac gac aag aag gaa tat ttc atc tagaggcgcc tgcccacttc ctgcgccccc  1380
Asp Asp Lys Lys Glu Tyr Phe Ile
                395

caggggccct gtggggactg ctggggccgt caccaacccg gacttgtaca gagcaaccgc 1440

agggccgccc ctcccgcttg ctccccagcc cacccacccc cctgtacaga atgtctgctt 1500

tgggtgcggt tttgtactcg gtttggaatg gggagggagg agggcggggg gaggggaggg 1560

ttgccctcag ccctttccgt ggcttctctg catttgggtt attattattt ttgtaacaat 1620

cccaaatcaa atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa 1680

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<210> 10
<211> 398
<212> PRT
<213> Homo sapien

<400> 10

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Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Leu Phe Ala
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Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
            20                  25                  30

Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
        35                  40                  45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
    50                  55                  60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
65                  70                  75                  80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
                85                  90                  95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
            100                 105                 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
        115                 120                 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
    130                 135                 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
145                 150                 155                 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
                165                 170                 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
            180                 185                 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
        195                 200                 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
    210                 215                 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
225                 230                 235                 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
                245                 250                 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
            260                 265                 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
        275                 280                 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
    290                 295                 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
305                 310                 315                 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
                325                 330                 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
            340                 345                 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
```

```
        355                 360                 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
    370                 375                 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
385                 390                 395
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